

OIEPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/851,873

DATE: 05/23/2001

TIME: 13:14:10

Input Set : A:\00233.txt

Output Set: C:\CRF3\05232001\I851873.raw

4 <110> APPLICANT: Kletzien, Rolf F
 5 Reardon, Ilene M
 6 Weiland, Katherine L
 8 <120> TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
 10 <130> FILE REFERENCE: 28341/00233
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/851,873
 C--> 13 <141> CURRENT FILING DATE: 2001-05-08
 15 <160> NUMBER OF SEQ ID NOS: 105
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1026
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapien
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(372)
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 30 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 31 1 5 10 15
 33 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa 96
 34 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 35 20 25 30
 37 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta 144
 38 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 39 35 40 45
 41 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
 42 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 43 50 55 60
 45 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
 46 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 47 65 70 75 80
 49 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
 50 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
 51 85 90 95
 53 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
 54 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 55 100 105 110
 57 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac 382
 58 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
 59 115 120
 61 ttgaaaacct tggatactca gtggttataa aagagaatct cacagctcag gaaatggaaa 442
 63 cagcactaag gcagtttgct gtcacccag agcaccagtc ctgagacagc acattcctgg 502
 65 tgtttatgtc acatagcatc ctgaatggaa tctgtgggac caagcactgg gatcaagagc 562
 67 cagatgttct tcacgatgac accatctttg aaattttcaa caaccgtaac tgccagagtc 622
 69 tgaaagacaa acccaaggtc atcatcatgc aagcctgccg aggcaatggt gctgggattg 682
 71 tttggttcac cactgacagt ggaaaagcca gtgcagatac tcatggtcgg ctcttgcaag 742

ENTERED

See p.5

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73 gtaacatctg taatgatgct gttacaaagg ctcatgtgga aaaggacttc attgctttca 802
75 aatcttccac accacataat gtttcttgga gacatgaaac aaatggctct gtcttcattt 862
77 cccaaattat ctactacttc agagagtatt cttggagtca tcatctagag gaaatttttc 922
79 aaaaggttca acattcattt gagaccccaa atatactgac ccagctgccc accattgaaa 982
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84 <210> SEQ ID NO: 2

85 <211> LENGTH: 124

86 <212> TYPE: PRT

87 <213> ORGANISM: Homo sapiens

89 <400> SEQUENCE: 2

90 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys

91 1 5 10 15

93 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu

94 20 25 30

96 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu

97 35 40 45

99 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu

100 50 55 60

102 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser

103 65 70 75 80

105 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala

106 85 90 95

108 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His

109 100 105 110

111 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met

112 115 120

115 <210> SEQ ID NO: 3

116 <211> LENGTH: 1026

117 <212> TYPE: DNA

118 <213> ORGANISM: Homo sapiens

120 <220> FEATURE:

121 <221> NAME/KEY: CDS

122 <222> LOCATION: (1)..(1023)

123 <223> OTHER INFORMATION:

125 <220> FEATURE:

126 <221> NAME/KEY: misc_feature /

127 <222> LOCATION: (373)..(374)..(375)

128 <223> OTHER INFORMATION: n = a or t or g or c

130 <220> FEATURE:

131 <221> NAME/KEY: misc_feature

132 <222> LOCATION: (125)

133 <223> OTHER INFORMATION: Xaa = any amino acid or no amino acid

135 <400> SEQUENCE: 3

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137 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys

138 1 5 10 15

140 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa 96

141 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu

142 20 25 30

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144 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta 144
145 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
146          35          40          45
148 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
149 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
150          50          55          60
152 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
153 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
154 65          70          75          80
156 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
157 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
158          85          90          95
160 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
161 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
162          100          105          110
W--> 164 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg nnn gat cta ctt 384
W--> 165 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Xaa Asp Leu Leu
166          115          120          125
168 gaa aac ctt gga tac tca gtg gtt ata aaa gag aat ctc aca gct cag 432
169 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
170          130          135          140
172 gaa atg gaa aca gca cta agg cag ttt gct gct cac cca gag cac cag 480
173 Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln
174 145          150          155          160
176 tcc tca gac agc aca ttc ctg gtg ttt atg tca cat agc atc ctg aat 528
177 Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn
178          165          170          175
180 gga atc tgt ggg acc aag cac tgg gat caa gag cca gat gtt ctt cac 576
181 Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His
182          180          185          190
184 gat gac acc atc ttt gaa att ttc aac aac cgt aac tgc cag agt ctg 624
185 Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu
186          195          200          205
188 aaa gac aaa ccc aag gtc atc atc atg caa gcc tgc cga ggc aat ggt 672
189 Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly
190          210          215          220
192 gct ggg att gtt tgg ttc acc act gac agt gga aaa gcc agt gca gat 720
193 Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp
194 225          230          235          240
196 act cat ggt cgg ctc ttg caa ggt aac atc tgt aat gat gct gtt aca 768
197 Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr
198          245          250          255
200 aag gct cat gtg gaa aag gac ttc att gct ttc aaa tct tcc aca cca 816
201 Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro
202          260          265          270
204 cat aat gtt tct tgg aga cat gaa aca aat ggc tct gtc ttc att tcc 864
205 His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser
206          275          280          285
208 caa att atc tac tac ttc aga gag tat tct tgg agt cat cat cta gag 912

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209 Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu
210      290      295      300
212 gaa att ttt caa aag gtt caa cat tca ttt gag acc cca aat ata ctg 960
213 Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu
214 305      310      315      320
216 acc cag ctg ccc acc att gaa aga cta tcc atg aca cga tat ttc tat 1008
217 Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr
218      325      330      335
220 ctc ttt cct ggg aat taa 1026
221 Leu Phe Pro Gly Asn
222      340
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 341
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: 125
233 <223> OTHER INFORMATION: Xaa = any amino acid or no amino acid
235 <400> SEQUENCE: 4
236 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
237 1      5      10      15
239 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
240      20      25      30
242 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
243      35      40      45
245 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
246      50      55      60
248 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
249 65      70      75      80
251 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
252      85      90      95
255 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
256      100      105      110
W--> 258 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Xaa Asp Leu Leu
259      115      120      125
261 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
262      130      135      140
264 Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln
265 145      150      155      160
268 Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn
269      165      170      175
271 Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His
272      180      185      190
274 Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu
275      195      200      205
277 Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly
278      210      215      220
280 Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp

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281 225          230          235          240
283 Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr
284          245          250          255
286 Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro
287          260          265          270
289 His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser
290          275          280          285
292 Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu
293          290          295          300
295 Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu
296 305          310          315          320
298 Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr
299          325          330          335
301 Leu Phe Pro Gly Asn
302          340
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 915
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (1)..(372)
318 <400> SEQUENCE: 5
319 atg gct gat gag aaa cca tcc aac ggt gtt ctg gtc cac atg gtg aag 48
320 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
321 1 5 10 15
323 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa 96
324 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
325 20 25 30
327 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta 144
328 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
329 35 40 45
331 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
332 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
333 50 55 60
335 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
336 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
337 65 70 75 80
339 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
340 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
341 85 90 95
343 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
344 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
345 100 105 110
347 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac 382
348 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
349 115 120
351 ttgaaaacct tggataactca gtggttataa aagagaatct cacagctcag gaaatggaaa 442
353 cagcactaag gcagtttgc tctcaccag agcaccagtc ctgagacagc acatttctgg 502

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/851,873

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Input Set : A:\00233.txt

Output Set: C:\CRF3\05232001\I851873.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55